

826

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/530,40/A  
Source: per  
Date Processed by STIC: 1/26/06

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## RAW SEQUENCE LISTING

DATE: 01/26/2006

PATENT APPLICATION: US/10/530,401A

TIME: 09:34:18

Input Set : A:\81356240.APP

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3 <110> APPLICANT: TANAKA, MANAMI
4   TANAKA, TOMOO
6 <120> TITLE OF INVENTION: CHIMERIC MOUSE WITH SUPPRESSED BRADEION GENE EXPRESSION
8 <130> FILE REFERENCE: 081356-0240
10 <140> CURRENT APPLICATION NUMBER: 10/530,401A
11 <141> CURRENT FILING DATE: 2005-04-07
13 <150> PRIOR APPLICATION NUMBER: PCT/JP02/010599
14 <151> PRIOR FILING DATE: 2002-10-11
16 <160> NUMBER OF SEQ ID NOS: 7
18 <170> SOFTWARE: PatentIn Ver. 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1649
22 <212> TYPE: DNA
23 <213> ORGANISM: Mus musculus
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26 <221> NAME/KEY: CDS
27 <222> LOCATION: (36)..(1469)
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32                               1           5
34 tgg caa ggg aac tct gtc ccc gag gac ggg act gaa gct ggg atc aag      101
35 Trp Gln Gly Asn Ser Val Pro Glu Asp Gly Thr Glu Ala Gly Ile Lys
36           10           15           20
38 cac ttc ctg gag gac agc agt gat gat gct gag ctg agc aag ttc gtg      149
39 His Phe Leu Glu Asp Ser Ser Asp Asp Ala Glu Leu Ser Lys Phe Val
40           25           30           35
42 aag gat ttc cca gga agc gaa ccc tac cac tca gcg gag tcc aag aca      197
43 Lys Asp Phe Pro Gly Ser Glu Pro Tyr His Ser Ala Glu Ser Lys Thr
44           40           45           50
46 agg gtg gcc agg ccc cag atc ttg gag cca agg ccc cag agc cca gac      245
47 Arg Val Ala Arg Pro Gln Ile Leu Glu Pro Arg Pro Gln Ser Pro Asp
48 55           60           65           70
50 ctc tgt gat gat gac gtg gag ttt aga ggc tcc ttg tgg ccc cag ccc      293
51 Leu Cys Asp Asp Asp Val Glu Phe Arg Gly Ser Leu Trp Pro Gln Pro
52           75           80           85
54 tct gac agt cag cag tac ttc agt gcc cca gcc cct ctc agc cct tcc      341
55 Ser Asp Ser Gln Gln Tyr Phe Ser Ala Pro Ala Pro Leu Ser Pro Ser
56           90           95           100
58 tcc agg ccc cgc agt cca tgg ggc aag ctt gat cct tat gat tcc tct      389
59 Ser Arg Pro Arg Ser Pro Trp Gly Lys Leu Asp Pro Tyr Asp Ser Ser
60           105           110           115
62 gag gat gac aag gag tat gtg ggc ttt gca acc ctc ccc aat caa gtc      437

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66 cac agg aag tct gtg aag aaa ggc ttt gac ttt aca ctc atg gtg gca 485
67 His Arg Lys Ser Val Lys Lys Gly Phe Asp Phe Thr Leu Met Val Ala
68 135      140      145      150
70 gga gaa tct ggt ctg ggt aaa tcc act ctt gtc aac agc ctc ttc ctc 533
71 Gly Glu Ser Gly Leu Gly Lys Ser Thr Leu Val Asn Ser Leu Phe Leu
72      155      160      165
74 act gac ttg tac cgg gat cgg aaa ctg ctg ggc gcc gaa gag cgg atc 581
75 Thr Asp Leu Tyr Arg Asp Arg Lys Leu Leu Gly Ala Glu Glu Arg Ile
76      170      175      180
78 atg caa acc gtg gag att act aag cac gca gtg gat ata gaa gag aag 629
79 Met Gln Thr Val Glu Ile Thr Lys His Ala Val Asp Ile Glu Glu Lys
80      185      190      195
82 gga gtg agg ctg cgg ctc acc att gtg gac act cca gga ttt ggg gat 677
83 Gly Val Arg Leu Arg Leu Thr Ile Val Asp Thr Pro Gly Phe Gly Asp
84      200      205      210
86 gca gtc aac aac aca gag tgc tgg aag cct gtg gcc gaa tac atc gac 725
87 Ala Val Asn Asn Thr Glu Cys Trp Lys Pro Val Ala Glu Tyr Ile Asp
88 215      220      225      230
90 cag cag ttt gag cag tac ttc cga gac gag agt ggc ctg aac cgc aag 773
91 Gln Gln Phe Glu Gln Tyr Phe Arg Asp Glu Ser Gly Leu Asn Arg Lys
92      235      240      245
94 aac atc cag gac aac cgg gtg cac tgc tgc ctg tac ttc atc tcc ccg 821
95 Asn Ile Gln Asp Asn Arg Val His Cys Cys Leu Tyr Phe Ile Ser Pro
96      250      255      260
98 ttt ggc cac ggg ctc cgg cca ttg gat gtt gaa ttc atg aag gcc ctg 869
99 Phe Gly His Gly Leu Arg Pro Leu Asp Val Glu Phe Met Lys Ala Leu
100      265      270      275
102 cat cag cgg gtc aac att gtg cct atc ttg gct aag gcg gac aca ctg 917
103 His Gln Arg Val Asn Ile Val Pro Ile Leu Ala Lys Ala Asp Thr Leu
104      280      285      290
106 acg cct cct gaa gtg gac cga aag aaa tgc aaa atc cgg gag gag atc 965
107 Thr Pro Pro Glu Val Asp Arg Lys Lys Cys Lys Ile Arg Glu Glu Ile
108 295      300      305      310
110 gag cac ttt gga atc aag atc tat cag ttc cca gac tgt gat tcc gat 1013
111 Glu His Phe Gly Ile Lys Ile Tyr Gln Phe Pro Asp Cys Asp Ser Asp
112      315      320      325
114 gag gac gag gac ttc aaa tta cag gac caa gcc cta aag gaa agc atc 1061
115 Glu Asp Glu Asp Phe Lys Leu Gln Asp Gln Ala Leu Lys Glu Ser Ile
116      330      335      340
118 cca ttt gcg gtg att ggc agc aac act gtg gta gaa gcc agg ggg cgg 1109
119 Pro Phe Ala Val Ile Gly Ser Asn Thr Val Val Glu Ala Arg Gly Arg
120      345      350      355
122 aga gtt cga ggc cgc ctc tac cct tgg ggc atc gtg gaa gtg gaa aac 1157
123 Arg Val Arg Gly Arg Leu Tyr Pro Trp Gly Ile Val Glu Val Glu Asn
124      360      365      370
126 cca ggt cac tgc gac ttt gtc aag ttg agg acg atg ctg gtg cgt acc 1205
127 Pro Gly His Cys Asp Phe Val Lys Leu Arg Thr Met Leu Val Arg Thr

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128 375          380          385          390
130 cac atg cag gac cta aag gat gtg acc cga gag aca cac tac gag aac 1253
131 His Met Gln Asp Leu Lys Asp Val Thr Arg Glu Thr His Tyr Glu Asn
132          395          400          405
134 tac agg gca cag tgt atc cag agc atg acc cgg cta gta gtg aag gaa 1301
135 Tyr Arg Ala Gln Cys Ile Gln Ser Met Thr Arg Leu Val Val Lys Glu
136          410          415          420
138 cgg aat cgc aac aaa ctg aca aga gag agt ggt act gac ttc cct atc 1349
139 Arg Asn Arg Asn Lys Leu Thr Arg Glu Ser Gly Thr Asp Phe Pro Ile
140          425          430          435
142 cct gct gtc cca cca ggg aca gat cca gaa act gag aag cta atc cgg 1397
143 Pro Ala Val Pro Pro Gly Thr Asp Pro Glu Thr Glu Lys Leu Ile Arg
144          440          445          450
146 gag aaa gac gaa gag ctg cgg cgg atg cag gag atg tta cac aaa atc 1445
147 Glu Lys Asp Glu Glu Leu Arg Arg Met Gln Glu Met Leu His Lys Ile
148 455          460          465          470
150 caa aga cag atg aag gag act cac taactggcctt ttggacctga atatttaa 1499
151 Gln Arg Gln Met Lys Glu Thr His
152          475
154 ctcttcttcc tgcctatgcc agcctctatt ccctgcatca gctctgctca ggaccccccg 1559
156 cagctcctac cagttcgctt tatatccctg ctgacttctc aagagactca gaggaataa 1619
158 actaacctat atgtggcaaa aaaaaaaaaa 1649
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163 <212> TYPE: DNA
164 <213> ORGANISM: Mus musculus
166 <400> SEQUENCE: 2
167 agccaaggcc ccagagccca gacctctgtg atgatgacgt ggagtttaga ggctccttgt 60
168 ggccccagcc ctctgacagt cagcagtact tcagtgtccc agccctctc agcccttct 120
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172 <210> SEQ ID NO: 3
173 <211> LENGTH: 171
174 <212> TYPE: DNA
175 <213> ORGANISM: Mus musculus
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178 agacgagagt ggcctgaacc gcaagaacat ccaggacaac cgggtgcact gctgcctgta 60
179 cttcatctcc ccgtttggcc acgggctccg gccattggat gttgaattca tgaaggccct 120
180 gcatcagcgg gtcaacattg tgcctatctt ggctaaggcg gacacactga c 171
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 191
185 <212> TYPE: DNA
186 <213> ORGANISM: Mus musculus
188 <400> SEQUENCE: 4
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190 tctgtgtgag gacccttgcc tggagataaa gttacaccta gagcgtgctg acaggggtct 120
191 caagtgtggg gcattggacca ttcactggga tggcaaggga actctgtccc cgaggacggg 180
192 actgaagctg g 191
195 <210> SEQ ID NO: 5
196 <211> LENGTH: 2225

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210 <222> LOCATION: (721)..(2225)
212 <400> SEQUENCE: 5
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215 ctagagcttt ctgacaggga gtctgaagcg tgggac atg gac cgt tca ctg gga 114
216                                     Met Asp Arg Ser Leu Gly
217                                     1           5
219 tgg caa ggg aat tct gtc cct gag gac agg act gaa gct ggg atc aag 162
220 Trp Gln Gly Asn Ser Val Pro Glu Asp Arg Thr Glu Ala Gly Ile Lys
221                                     10           15           20
223 cgt ttc ctg gag gac acc acg gat gat gga gaa ctg agc aag ttc gtg 210
224 Arg Phe Leu Glu Asp Thr Thr Asp Asp Gly Glu Leu Ser Lys Phe Val
225                                     25           30           35
227 aag gat ttc tca gga aat gcg agc tgc cac cca cca gag gct aag acc 258
228 Lys Asp Phe Ser Gly Asn Ala Ser Cys His Pro Pro Glu Ala Lys Thr
229                                     40           45           50
231 tgg gca tcc agg ccc caa gtc ccg gag cca agg ccc cag gcc ccg gac 306
232 Trp Ala Ser Arg Pro Gln Val Pro Glu Pro Arg Pro Gln Ala Pro Asp
233 55           60           65           70
235 ctc tat gat gat gac ctg gag ttc aga ccc ccc tcg cgg ccc cag tcc 354
236 Leu Tyr Asp Asp Asp Leu Glu Phe Arg Pro Pro Ser Arg Pro Gln Ser
237                                     75           80           85
239 tct gac aac cag cag tac ttc tgt gcc cca gcc cct ctc agc cca tct 402
240 Ser Asp Asn Gln Gln Tyr Phe Cys Ala Pro Ala Pro Leu Ser Pro Ser
241                                     90           95           100
243 gcc agg ccc cgc agc cca tgg ggc aag ctt gat ccc tat gat tcc tct 450
244 Ala Arg Pro Arg Ser Pro Trp Gly Lys Leu Asp Pro Tyr Asp Ser Ser
245                                     105          110          115
247 gag gta gag cct cca gcc ctg cct ttg cct ttc agt ggg ctg ctg cag 498
248 Glu Val Glu Pro Pro Ala Leu Pro Leu Pro Phe Ser Gly Leu Leu Gln
249                                     120          125          130
251 gaa gac cgg ggg cag gga gca gag tgt gtg tgt gtg tgt gtg tgt gtg 546
252 Glu Asp Arg Gly Gln Gly Ala Glu Cys Val Cys Val Cys Val Cys Val
253 135          140          145          150
255 tgt gtg tgt gtg tgt ttg tgt gtg tgt gta tct ggg acc tat ttc agt 594
256 Cys Val Cys Val Cys Leu Cys Val Cys Val Ser Gly Thr Tyr Phe Ser
257                                     155          160          165
259 cct gtg tca gcc cta gct cca aga tat ctg ccc cca agg gca ctg gaa 642
260 Pro Val Ser Ala Leu Ala Pro Arg Tyr Leu Pro Pro Arg Ala Leu Glu
261                                     170          175          180

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263 att tgc agt ttc agc aag ggc agg agg ccc agc tgg tgg cct cag atg      690
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265          185                      190                      195
267 gga act cac aga agt ctg gca ctg ctt ttt taaggctggg gcaaaggcct      740
268 Gly Thr His Arg Ser Leu Ala Leu Leu Phe
269      200                      205
271 gaaagggaga gaagattggc gctgggtgcc ggggcccctt tggctcctca ccgtgatgca 800
273 ttctgccttc ctgtctacta ggatgacaag gagtatgtgg gctttgcaac cctccccaac 860
275 caagtccacc gaaagtccgt gaagaaaaggc tttgacttta ccctcatggg ggcaggagag 920
277 tctggcctgg gcaaatccac acttgtcaat agcctcttcc tactgatct gtaccgggac 980
279 cggaaacttc ttggtgctga agagaggatc atgcaaaactg tggagatcac taagcatgca 1040
281 gtggacatag aagagaaggg tgtgaggctg cggctcacca ttgtggacac accaggtttt 1100
283 ggggatgcag tcaacaacac agagtgtctg aagcctgtgg cagaatacat tgatcagcag 1160
285 tttgagcagt atttccgaga cgagagtggc ctgaaccgaa agaacatcca agacaacagg 1220
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309 ccttttctcc ctttagcaaa ctgactcggg aaagtgttac cgacttcccc atccctgctg 1940
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313 ggcggatgca ggagatgcta cacaaaatac aaaaacagat gaaggagaac tattaactgg 2060
315 ctttcagccc tggatattta aatctcctcc tcttcttct gtccatgccg gccctccca 2120
317 gcaccagctc tgtcaggcc ccttcagcta ctgccacttc gccttacatc cctgctgact 2180
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332          20          25          30
334 Glu Leu Ser Lys Phe Val Lys Asp Phe Pro Gly Ser Glu Pro Tyr His
335          35          40          45
337 Ser Ala Glu Ser Lys Thr Arg Val Ala Arg Pro Gln Ile Leu Glu Pro
338          50          55          60
340 Arg Pro Gln Ser Pro Asp Leu Cys Asp Asp Asp Val Glu Phe Arg Gly
341  65          70          75          80
343 Ser Leu Trp Pro Gln Pro Ser Asp Ser Gln Gln Tyr Phe Ser Ala Pro
344          85          90          95
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**VERIFICATION SUMMARY**

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